Useful list of typed commands for XWIN-NMR 3.5 and Topspin 1.3

Revised October 2008

Command	Action
a	opens the acquisition window for observing the accumulation of the FID during acquisition
abs	performs a baseline correction on the acquired spectrum, ie flattens the baseline
apk	performs an automatic phase correction on the acquired spectrum
ased	opens the truncated acquisition parameters for editing pulse sequence parameters, such as relaxation delays, pulse widths etc.
bsmsdisp	"Bruker Smart Magnet System Display" opens the controls for sample and shims
d1	relaxation delay
eda	opens the complete acquisition parameters for editing parameters - used by experienced users for changing spectral windows and acquisition times for 2D experiments
efp	performs a Fourier transfer of the FID using a line broadening given by lb (in Hz)
ft	performs a Fourier transfer of the FID without using a line broadening given by lb (in Hz)
gpro	"get probe-solvent table" – (use **getprosol** in Topspin) updates the parameter set with correct pulse sequence delays and pulse widths for your experiment of choice
halt	stops the experiment after finishing the current phase cycle (multiple of 4 scans) and transfers (saves) data to your dataset
ii	"initial experiment" an old command no longer necessary for setting up a new experiment - can be used after **rpar** and **gpro**
lock	sets the lock frequency to match the ^{2}D frequency of the solvent chosen
lockdisp	opens the lock display
new	displays the dataset parameters – user inputs the name and file path to which the NMR data is stored
ns	"number of scans" change the numbers of scans before user types zg; must be a multiple of four
o1p	center chemical shift (ppm) of the spectrum acquired
rpar	"read parameter set" lists all the parameters sets available (only some are OSU installed and optimized) - only use those which you have been specifically trained
rsh	"read shim" - when typed alone this command will list all the saved shim files OR may follow command with shim file ie **rsh QNPtly**
sr	after referencing the solvent peak to a specific chemical shift - this value is the difference (in Hz) of the shift
stop	stops the experiment immediately and does not transfer (or save) the data
sw	spectral window or width in ppm of the spectrum acquired
tr	transfers files to your dataset after finishing the current phase cycle (multiple of 4 scans)
wobb	starts the tuning interface
xwinplot	opens the Plot Editor